Gleason score in the subject, wherein the PSA levels and/or Gleason score is used in combination with the signature score to select a therapy.

61. The method of claim **54**, wherein the cancer is prostate cancer or estrogen receptor-positive breast cancer.

62. The method of claim **54**, wherein measuring the expression level comprises using at least one primer pair and/or at least one probe that hybridizes with the at least one gene.

63. The method of claim **54**, wherein the pre-determined threshold scored is obtained by measuring an expression level of the at least one gene in one or more control samples.

64. The method of claim **54**, wherein the expression level is measured by microarray, northern blotting, RNA sequencing, in situ RNA detection or nucleic acid amplification.

65. The method of claim **54**, wherein the sample comprises (i) prostate cells and/or prostate tissue or (ii) breast cells and/or breast tissue.

66. The method of claim **54**, wherein the sample is a formalin-fixed paraffin-embedded biopsy sample or a resection sample.

67. A system for characterizing and/or prognosing cancer in a subject, comprising:

(a) one or more testing devices for measuring an expression level of at least one gene selected from CAP6, THBS4, PLP1, MT1A, MIR205HG, SEMG1, RSPO3, AN07, PCP4, ANKRD1, MYBPC, MMP7, SERPINA3, SELE, KRT5, LTF, KIAA120, TMEM158, ZFP36, FOSB, PCA3, TRPM8, PTTG1, PAGE4, STEAP4, TMEM178A, CXCL2, HS3ST3A1, EYA1, RSPO2, PKP1, MUC6, PENK, DEFB1, SLC7A3, MIR578, PI15, UBXN10-AS1, PDK4, PHGR1, SERPINE1, PDZRN4, ZNF185, ADRA2C, AZGP1, TK1, POTEH, KIF11, CLDN1, MIR4530, MAFF, ZNF765, CKS2, TCEAL7, PLIN1, SIGLEC1, FAM15, MFAP5, SFRP1, DUSP5, VARS2, ABCC4, SH3BP4, SORD, MTERFD1, DPP4, FAM3B, KLK3, a gene comprising anyone of SEQ ID NOs: 32, 96, 97, 112-114, 120, 121, 132, 141, 149, 185, 186, 210, 211, 213, 214, 221, 264, 328, 329, 344-346, 352, 353, 364, 373, 381, 417, 418, 442, 443, 445, 446 and 453, and a gene comprising any one of SEQ ID NOs: 133 and 365, in a sample from a subject;

(b) a storage medium comprising instructions; and

(c) a processor configured to execute the instructions to perform operations comprising:

(i) accessing from the one or more testing devices the measured expression level of the at least one gene;

(ii) providing a signature score based on the measured expression level, wherein the signature score is

a single signature score if the at least one gene consists of one gene, or

a combined signature score if the at least one gene consists of two or more genes;

(iii) determining if the signature score is a positive signature score, wherein the signature score is a positive signature score if

the single signature score is higher than a gene with a positive weight,

the single signature score is lower than a gene with a negative weight, or

the combined signature score is equal to or higher than a pre-determined threshold score;

wherein a positive signature score indicates an increased likelihood of recurrence and/or an increased likelihood of metastasis and/or a poor prognosis;

(iv) outputting the positive signature score.

68. The system of claim **67**, further comprising a display for outputting the positive signature score.

69. A kit for characterizing and/or prognosing cancer in a subject comprising one or more oligonucleotide probes that specifically hybridize with a full sequence, a target sequence, or an RNA product of at least one gene selected from CAP6, THBS4, PLP1, MT1A, MIR205HG, SEMG1, RSPO3, AN07, PCP4, ANKRD1, MYBPC, MMP7, SERPINA3, SELE, KRT5, LTF, KIAA120, TMEM158, ZFP36, FOSB, PCA3, TRPM8, PTTG1, PAGE4, STEAP4, TMEM178A, CXCL2, HS3ST3A1, EYA1, RSPO2, PKP1, MUC6, PENK, DEFB1, SLC7A3, MIR578, PI15, UBXN10-AS1, PDK4, PHGR1, SERPINE1, PDZRN4, ZNF185, ADRA2C, AZGP1, TK1, POTEH, KIF11, CLDN1, MIR4530, MAFF, ZNF765, CKS2, TCEAL7, PLIN1, SIGLEC1, FAM15, MFAP5, SFRP1, DUSP5, VARS2, ABCC4, SH3BP4, SORD, MTERFD1, DPP4, FAM3B, KLK3, a gene comprising any one of SEQ ID NOs: 32, 96, 97, 112-114, 120, 121, 132, 141, 149, 185, 186, 210, 211, 213, 214, 221, 264, 328, 329, 344-346, 352, 353, 364, 373, 381, 417, 418, 442, 443, 445, 446 and 453, and a gene comprising any one of SEQ ID NOs: 133 and 365, and further comprising one or more of:

a) a blocking probe,

b) a pre-amplifier,

c) an amplifier, and

d) a label molecule.

70. The kit of claim **69**, wherein the at least one gene consists of all of CAP6, THBS4, PLP1, MT1A, MIR205HG, SEMG1, RSPO3, AN07, PCP4, ANKRD1, MYBPC, MMP7, SERPINA3, SELE, KRT5, LTF, KIAA120, TMEM158, ZFP36, FOSB, PCA3, TRPM8, PTTG1, PAGE4, STEAP4, TMEM178A, CXCL2, HS3ST3A1, EYA1, RSPO2, PKP1, MUC6, PENK, DEFB1, SLC7A3, MIR578, PI15, UBXN10-AS1, PDK4, PHGR1, SERPINE1, PDZRN4, ZNF185, ADRA2C, AZGP1, TK1, POTEH, KIF11, CLDN1, MIR4530, MAFF, ZNF765, CKS2, TCEAL7, PLIN1, SIGLEC1, FAM15, MFAP5, SFRP1, DUSP5, VARS2, ABCC4, SH3BP4, SORD, MTERFD1, DPP4, FAM3B, KLK3, a gene comprising any one of SEQ ID NOs: 32, 96, 97, 112-114, 120, 121, 132, 141, 149, 185, 186, 210, 211, 213, 214, 221, 264, 328, 329, 344-346, 352, 353, 364, 373, 381, 417, 418, 442, 443, 445, 446 and 453, and a gene comprising any one of SEQ ID NOs: 133 and 365.

71. The kit of claim **69**, further comprising one or more primers and/or primer pairs for amplifying the full sequence or the target sequence of the at least one gene.

72. The kit of claim **71**, wherein the one or more primer and/or primer pair comprise at least one nucleotide sequence selected from SEQ ID NOs: 3015-3154.

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